



## RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/677, 956B  
Source: TEFW/6  
Date Processed by STIC: 09/14/2006

**ENTERED**



IFW16

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/677,956B DATE: 09/14/2006  
TIME: 15:32:14

Input Set : E:\16988.ST25.txt  
Output Set: N:\CRF4\09142006\J677956B.raw

5 <110> APPLICANT: Zebedee, Suzanne  
6 Inchauspe, Genevieve  
7 Nasoff, Marc S.  
8 Prince, Alfred M.  
10 <120> TITLE OF INVENTION: METHODS AND SYSTEMS FOR PRODUCING RECOMBINANT  
VIRAL ANTIGENS  
12 <130> FILE REFERENCE: 323-100USD  
14 <140> CURRENT APPLICATION NUMBER: 10/677,956B  
15 <141> CURRENT FILING DATE: 2003-10-01  
17 <150> PRIOR APPLICATION NUMBER: 08/931,855  
18 <151> PRIOR FILING DATE: 1997-09-16  
20 <150> PRIOR APPLICATION NUMBER: 08/563,733  
21 <151> PRIOR FILING DATE: 1995-11-08  
23 <150> PRIOR APPLICATION NUMBER: 08/272,271  
24 <151> PRIOR FILING DATE: 1994-07-08  
26 <150> PRIOR APPLICATION NUMBER: 07/616,369  
27 <151> PRIOR FILING DATE: 1990-11-21  
29 <150> PRIOR APPLICATION NUMBER: 07/573,643  
30 <151> PRIOR FILING DATE: 1990-08-27  
32 <160> NUMBER OF SEQ ID NOS: 74  
34 <170> SOFTWARE: PatentIn version 3.3  
36 <210> SEQ ID NO: 1  
37 <211> LENGTH: 795  
38 <212> TYPE: DNA  
39 <213> ORGANISM: Human immunodeficiency virus  
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43 <221> NAME/KEY: CDS  
44 <222> LOCATION: (16)..(789)  
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49 1 5 10  
51 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta 99  
52 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val  
53 15 20 25  
55 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147  
56 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu  
57 30 35 40  
59 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195  
60 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val  
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63 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243  
64 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu  
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68 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile	
69 80 85 90	
71 gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act	339
72 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr	
73 95 100 105	
75 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct	387
76 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro	
77 110 115 120	
79 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat	435
80 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn	
81 125 130 135 140	
83 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa	483
84 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln	
85 145 150 155	
87 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act	531
88 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr	
89 160 165 170	
91 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa	579
92 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu	
93 175 180 185	
95 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa	627
96 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys	
97 190 195 200	
99 gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag	675
100 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln	
101 205 210 215 220	
103 gga gta gga gga ccc aaa aat caa caa tta tta tcc tta tgg ggg tgt	723
104 Gly Val Gly Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys	
105 225 230 235	
107 aaa ggg aaa ctt gtt tgt tat act tcc gtt aaa tgg aat gga ccc ggc	771
108 Lys Gly Lys Leu Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly	
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119 <213> ORGANISM: Human immunodeficiency virus	
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128 20 25 30	
131 Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala	
132 35 40 45	
135 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln	
136 50 55 60	

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Input Set : E:\16988.ST25.txt  
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139 Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu  
140 65 70 75 80  
143 Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln  
144 85 90 95  
147 Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu  
148 100 105 110  
151 Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly  
152 115 120 125  
155 Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg  
156 130 135 140  
159 Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu  
160 145 150 155 160  
163 Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu  
164 165 170 175  
167 Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val  
168 180 185 190  
171 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro  
172 195 200 205  
175 Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly  
176 210 215 220  
179 Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys Lys Gly Lys Leu  
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183 Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly His Lys Ala Arg  
184 245 250 255  
187 Val Leu  
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192 <211> LENGTH: 795  
193 <212> TYPE: DNA  
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197 <220> FEATURE:  
198 <221> NAME/KEY: CDS  
199 <222> LOCATION: (16)..(789)  
201 <400> SEQUENCE: 3  
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203 Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val  
204 1 5 10  
206 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta 99  
207 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val  
208 15 20 25  
210 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147  
211 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu  
212 30 35 40  
214 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195  
215 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val  
216 45 50 55 60  
218 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag  
219 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu  
220 65 70 75  
222 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att 291

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227	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	
228				95				100				105					
230	act	agt	acc	ctt	cag	gaa	caa	ata	gga	tgg	atg	aca	aat	aat	cca	cct	387
231	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	
232				110				115				120					
234	atc	cca	gta	gga	gaa	att	tat	aaa	aga	tgg	ata	atc	ctg	gga	tta	aat	435
235	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	
236	125					130					135					140	
238	aaa	ata	gta	aga	atg	tat	agc	cct	acc	agc	att	ctg	gac	ata	aga	caa	483
239	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	
240					145				150			155					
242	gga	cca	aag	gaa	ccc	ttt	aga	gac	tat	gta	gac	cg	ttc	tat	aaa	act	531
243	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	
244					160				165			170					
246	cta	aga	gcc	gag	caa	gct	tca	cag	gag	gta	aaa	aat	tgg	atg	aca	gaa	579
247	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	
248					175				180			185					
250	acc	ttt	ttg	gtc	caa	aat	gcg	aac	cca	gat	tgt	aag	act	att	tta	aaa	627
251	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	
252					190				195			200					
254	gca	ttg	gga	cca	gcg	gct	aca	cta	gaa	gaa	atg	atg	aca	gca	tgt	cag	675
255	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	
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258	gga	gta	gga	gga	ccc	aaa	aat	caa	caa	aga	tta	aat	tta	tgg	ggg	tgt	723
259	Gly	Val	Gly	Gly	Pro	Lys	Asn	Gln	Gln	Arg	Leu	Asn	Leu	Trp	Gly	Cys	
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262	aaa	ggg	aaa	ctt	att	tgt	tat	act	tcc	gtt	aaa	tgg	aat	gga	ccc	ggc	771
263	Lys	Gly	Lys	Leu	Ile	Cys	Tyr	Thr	Ser	Val	Lys	Trp	Asn	Gly	Pro	Gly	
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286	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	
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303																
306	100								105							110
307	115								120							125
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311																
314	130								135							140
315	145								150							160
318	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu
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322	165								170							175
323	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val
326																
327	180								185							190
330	195								200							205
331	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly
334																
335	210								215							220
338	Pro	Lys	Asn	Gln	Gln	Arg	Leu	Asn	Leu	Trp	Gly	Cys	Lys	Gly	Lys	Leu
339																
342	225								230							235
346	Ile	Cys	Tyr	Thr	Ser	Val	Lys	Trp	Asn	Gly	Pro	Gly	His	Lys	Ala	Arg
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359	<222>	LOCATION:	(16)..(789)													
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367	15								20				25			
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373	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val
374																
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376	ggg	gga	cat	caa	gca	gcc	atg	caa	atg	tta	aaa	gag	acc	atc	aat	gag
377	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu
378																
379	65									70						75
380	gaa	gct	gca	gaa	tgg	gat	aga	gtg	cat	cca	gtg	cat	gca	ggg	cct	att
381	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile
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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/677,956B

DATE: 09/14/2006  
TIME: 15:32:15

Input Set : E:\16988.ST25.txt  
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Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/677,956B

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SEQUENCE LISTING

<110> Zebedee, Suzanne  
Inchauspe, Genevieve  
Nasoff, Marc S.  
Prince, Alfred M.  
<120> METHODS AND SYSTEMS FOR PRODUCING RECOMBINANT VIRAL ANTIGENS  
<130> 323-100USD  
<140> 10/677,956  
<141> 2003-10-01  
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<151> 1997-09-16  
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His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val  
15 20 25

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Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu  
30 35 40

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Page 1

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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
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